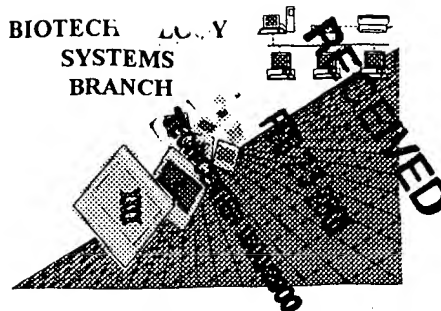


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECH  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/358,321B

Source: 1638

Date Processed by STIC: 2/8/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

1638

RAW SEQUENCE LISTING DATE: 02/08/2001  
 PATENT APPLICATION: US/09/358,321B TIME: 11:56:37

Input Set : A:\SubstituteSEQUENCE LISTING50447.txt  
 Output Set: N:\CRF3\02082001\I358321B.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Sukhapinda, Kitisri  
 4 Hasler, James M  
 5 Petell, James K  
 6 Strickland, James A  
 7 Folkerts, Otto  
 9 <120> TITLE OF INVENTION: ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS  
 11 <130> FILE REFERENCE: 50447  
 13 <140> CURRENT APPLICATION NUMBER: US 09/358,321B  
 14 <141> CURRENT FILING DATE: 1999-07-21  
 16 <150> PRIOR APPLICATION NUMBER: US 60/093,587  
 17 <151> PRIOR FILING DATE: 1998-07-21  
 E--> 19 <160> NUMBER OF SEQ ID NOS: 56 60 in file (see below)  
 21 <170> SOFTWARE: PatentIn Ver. 2.0

Suggestion:

Consult new

Sequence Rules  
 for format

#### ERRORED SEQUENCES

2027 <210> SEQ ID NO: 58  
 2028 <211> LENGTH: 12 15 shown  
 2029 <212> TYPE: DNA  
 2030 <213> ORGANISM: Artificial Sequence  
 2032 <220> FEATURE:  
 2033 <223> OTHER INFORMATION: Description of Artificial Sequence: putative N-terminus of the precursor protein  
 2035 <400> SEQUENCE: 58  
 E--> 2036 atggctagcctccgc 12 15  
 2039 <210> SEQ ID NO: 59  
 2040 <211> LENGTH: 12 4 shown  
 2041 <212> TYPE: PRT  
 2042 <213> ORGANISM: Zea Mays  
 2044 <400> SEQUENCE: 59  
 E--> 2045 Met/Ala/Leu/Arg 4 delete - amino acids are numbered under every 5 amino acids  
 2048 <210> SEQ ID NO: 60  
 2049 <211> LENGTH: 12 5 shown  
 2050 <212> TYPE: PRT  
 2051 <213> ORGANISM: Artificial Sequence  
 2053 <220> FEATURE:  
 2054 <223> OTHER INFORMATION: Description of Artificial Sequence: putative N-terminus of the precursor protein  
 2056 <400> SEQUENCE: 60  
 2057 Met/Ala/Ser/Leu/Arg insert 5 number 5 delete  
 E--> 2064 1  
 E--> 2067 34 delete at end of file

Per 1.822 of new sequence rules, group all non-coding bases into 10's, leaving one space between each group of 10 bases

last sequence in file

FYI:

#### Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 02/08/2001

PATENT APPLICATION: US/09/358,321B

TIME: 11:56:38

Input Set : A:\SubstituteSEQUENCE LISTING50447.txt

Output Set: N:\CRF3\02082001\I358321B.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2036 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:15 SEQ:58  
L:2036 M:252 E: No. of Seq. differs, <211>LENGTH:Input:12 Found:15 SEQ:58  
L:2045 M:252 E: No. of Seq. differs, <211>LENGTH:Input:12 Found:0 SEQ:59  
L:2064 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ-ID:60  
M:332 Repeated in SeqNo=60  
L:2067 M:252 E: No. of Seq. differs, <211>LENGTH:Input:12 Found:0 SEQ:60  
L:19 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (56) Counted (60)